

Amendments to the Specification:

Please replace the Sequence Listing printout and diskette filed on April 18, 2005 with the attached Sequence Listing printout and diskette enclosed herewith.

On page 7, please replace the paragraph starting on line 32 with the following:

Figure 3 depicts exemplary switchable promoter constructs (SEQ ID NOs:22-26 and 75, respectively) engineered to have a compound, ligand or drug binding sequence near *the cis* element, with the transcriptional regulatory protein DNA response element indicated as bolded and uppercase, the introduced nucleic acid sequence for compound binding indicated in lowercase and potential compound binding sequences indicated as () or []. In such constructs, the compound binding sequence may be introduced relative to the transcriptional regulatory protein DNA response element, in one or more locations including: (1) on either side, (2) on both sides, (3) upstream, (4) downstream, or (5) overlapping the DNA response element.

On page 47, please replace the paragraph starting on line 8 with the following:

AC(**TTTA**tttt) (SEQ ID NO:65)
(aaa**ACTT**TA) (SEQ ID NO:77)

On page 61, please replace the paragraph starting on line 32 with the following:

Site-directed mutagenesis of the -30 to -21 promoter region was carried out and constructs assayed in MCF7 cells. The assay results indicate that bases between -30 and -24 (GAGTTTT SEQ ID NO:76) are the most important for transcriptional activation from this site (Table 9).

On page 62, please replace Table 9 with the following:

Table 9 Reporter Activity Of Cyclin D1 Promoter Constructs

Construct	Mutations in -30-21 region	% Wild Type Activity
WT -1745	GAGTTTTGTT (SEQ ID NO: 71)	100
-30 -21 -1745	TCTGGGATCC (SEQ ID NO: 36)	33 +/- 2.2
-30 -26 -1745	TCTGGTTGTT (SEQ ID NO: 70)	43 +/- 3.5
-25 -21 -1745	GAGTTGGCGG (SEQ ID NO: 69)	34 +/- 4.7
-30 -28 -1745	TCTTTTGT (SEQ ID NO: 68)	33 +/- 6.3
-28 -23 -1745	GATGGGATTT (SEQ ID NO: 67)	46 +/- 5.1
-23 -21 -1745	GAGTTTTTCC (SEQ ID NO: 66)	138 +/- 16.4
10 bp 21x -1745	GAGTTTTTTTAAG (SEQ ID NO: 37)	87 +/- 11.4
8 bp 21x -1745	GAGTTTAAAAGAG (SEQ ID NO: 38)	85 +/- 7.8

On page 63, please replace Table 10 with the following:

Table 10. Reporter Analysis of Site-Directed Mutants of HNF3 and HNF4 Sites of the HBV Core Promoter.

	Nucleotide Coordinates (HBV ayw Strain)	Site-Directed Mutant Sequence	Percent Wild Type HepAD38
Distal HNF3	1680 - 1691	CCAGGGCCCCGA (SEQ ID NO: 72)	102
Proximal HNF3	1715 - 1726	GCCGCGGTCTGT (SEQ ID NO: 73)	33
HNF4	1661 - 1672	CGTCCGCGGTGA (SEQ ID NO: 74)	29

On pages 67-68, please replace the Sequence Listing table with the following:

SEQUENCE LISTING TABLE

(all oligonucleotides shown as single stranded in 5' to 3' direction)

Description	SEQ ID NO
UL9 DNA response element CGTTCGCACTT (11 bp)	1
GAL4 DNA response element CGGAGTACTGTCCTCCG (17 bp)	2
ZFHD1 DNA response element TAATTANGGGNG (12 bp)	3
NF-KB p65 Genbank Accession Number HUMP65NFKB	4
tetO DNA response element TCCCTATCAGTGATAGAGA (19 bp)	5
lacO DNA response element CTTAACACTCG:CGAGTGTTAAG (22 bp)	6
Ecdysone receptor RG(GT)TCANTGA(CA)CY (15 bp)	7
VP16: aa 413-489: TAPITDVSLGDELRLDGEEVDMTPADALDDFDLEMLGDVESPPGMTHDPVSYGALD VDDFEFEQMFTDALGIDDFG	8
VP64: tetramer of aa 437-447 of VP16: ADALDDFDLEMADALDDFDLEMADALDDFDLEMADALDDFDLEM	9
KRAB: aa 1-97 reference or sequence	10
Mad: aa 1-36 reference or sequence	11
Sequence of <i>rrnB</i> P1 promoter: from -66 to +50 CGCGGTCAGAAAATTATTTTAAATTTCTCTTGTCAGGCCGGAATAACTCCCTATAA TGCGCCACCACTGACACGGAACAACGGCAAACACGCCGCCGGGTCAGCGGGGTTCTC CT	12
<i>rrnB</i> P1 promoter UP element AGAAAATTATTTTAAATTTCT	13
RLG3097 (core) GACTGCAGTGGTACCTAGGAGG	14
RLG3074 (WILD TYPE) AG(AAAATTATTTTAAATTT)CCT	15
RLG4192 GG(AAAATTTTTCATTTTCAAAA)GTA	16
RLG4174 TG(AAATTTATTTT)GCGAAAGGG	17
modified UL-9 DNA response sequence TGTTCGCACTT	18
modified UL-9 DNA response sequence (YK 202LX, 52-mer) CATGGACG CCACTG AGCCGtttt TGTTCGCACTT GAGGCGAGTCGATGCACC	19
modified UL-9 DNA response sequence (YK 202RX-A, 54-mer) CATGGACG CCACTG AGCCG TGTTCGCACTT ttttttGAGGCGAGTCGATGCACC	20
modified UL-9 DNA response sequence (YK 202RX, 58-mer) CATGGACG CCACTG AGCCGTTTT TGTTCGCACTT ttttttGAGGCGAGTCGATGCACC	21
MEF C(TTAAAAATAA)C	22
780BP (TTGAAAAATCAA)CGCT	23
UL9 (modified) (ttttTGTT)CGCAC(TTtttttt)	24

NFkB (modified) (tttttGGG[AtTTT)CCTtttt]	25
LacO (modified) (aaaaAATT)GTGAGCGCTCAC(AATTtttt)	26
NtBBF1 (plant tissue-specific transcription factor) ACTTTA	27
DRE (plant element identified in the promoter region of the rd29A gene associated with dehydration and cold- induced gene expression) TACCGACAT	28
NF-kB DNA response sequence from Igk promoter: GGGACTTTCC	29
NF-kB DNA response sequence from IL-6 promoter: GGGATTTTCC	30
JF101 (NFkB1) (50mer) (right side) cgac cgtgctcgag TTAACGGGACTTTCCAAaaa cgatcg gact ggactc	31
JF 102 (NFkB2)(60mer)(right side) cgac cgtgctcgag TTAACGGGATTTTCCAAaaa cgatcg gact ggactc	32
JF 103 (NFkB3)(60mer) (both sides) cgac cgtgctcgag aaattGGGATTTTCCAAaaa cgatcg gact ggactc	33
LacI aaaaAATTGTGAGCGCTCACAATTtttt	34
LacI ttttttTTGTGAGCGGATAACAAaa	35
Cyclin D1 -30-21 TCTGGGATCC	36
Cyclin D1 10bp 21x GAGTTTTTTTTTAAG	37
Cyclin D1 8bp 21x GAGTTTTAAAGAG	38
NFkB p50 Genbank Accession Number HUMNFkB34	39
NFkB pMC3 (NheI to BglI) <u>GCTAGCCCCGCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTTAT</u> <u>ATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCAGATCT</u>	40
NFkB 2MC5 (NheI to BglI) <u>GCTAGCGCCCAAATTGGGATTTTCCAAAAAGCCGAAATTGGGATTTTCCAAAAACCG</u> <u>CCGATCGCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTTA</u> <u>TATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCAGATCT</u>	41
NFkB 4MC1 (MluII to BglI) <u>ACGCGTGCCCAAATTGGGATTTTCCAAAAAGCCGAAATTGGGATTTTCCAAAAACCG</u> <u>CGTAGCGCCCAAATTGGGATTTTCCAAAAAGCCGAAATTGGGATTTTCCAAAAACC</u> <u>GCCGATCGCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTTT</u> <u>ATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCAGATCT</u>	42
NFkB BKMC1 (NheI to BglI) <u>GCTAGCCCCGCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTTAT</u> <u>ATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCAGATCT</u>	43
NFkB BK2MC5 (NheI to BglI) <u>GCTAGCGCCAGGTCGGGATTTTCCGAGGAGCCGAGGTCGGGATTTTCCGAGGACCG</u> <u>CCGATCGCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGCCTA</u> <u>TATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCAGATCT</u>	44

BK2MC12 (NheI to BglI) <u>GCTAGCGCCAGGTCGGGATTTTCCGAGGAGCCGAGGTCGGGATTTTCCGAGGACCG</u> <u>CCGATCGCCCGCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGCCTA</u> <u>TATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCAGATCT</u>	45
NFKB SWCMV	46
NFKB MTCMV	47
NFKB BKCMV	48
HBV core proximal, HNF3-2 binding site (GACTGTTTGTTT)	49
HBV core HNF4 binding site (AGGACTCTTGGA)	50
HBV core WT TACTAGGAGGCTGTAGGCATAAATTGGTCTGCGCACCAGCACCATG	51
HBV core TATA21xR TACTAGGAGGCTGTAGGCATAAATTAGTCTGCGCACCAGCACCATG	52
HBV core TATAmut (TACTAGGATTAGTGCTTAAGCCCTTGGTCTGCGCACCAGCACCATG)	53
HBV core 3'TATAmut (TACTAGGAGGCTGTAGGCATAAAGCTCGAGTATACAACGCACCATG)	54
HBV core TATARds1 TACTAGGAGGCTGTAGGCATAAATGCGTAAAAGCACCAGCACCATGCAAC	55
HBV core TATARds2 TACTAGGAGGCTGTAGGCATAAATTAAAAACGCACCAGCACCATGCAAC	56
HBV core TATARds3 TACTAGGAGGCTGTAGGCATAAATTAATCCGCGCACCAGCACCATGCAAC	57
HNF3Rds1 ACCTTGAGGCATACTTCAAAGACTGTTGATTTAGCGAATAAGAGGAGTTGG	58
HNF3Rds2 ACCTTGAGGCATACTTCAAAGACTGTTTATTTAATAACGGGAGGAGTTGG	59
HNF3Rds3 ACCTTGAGGCATACTTCAAAGACTGTTTATTTAAGGACTGGGAGGAGTTGG	60
pACTULVP activator construct-Figs 14A/B	61
pACT ULKRAB repressor construct-Figs 15A/B	62
Herpes simplex virus type 2 VP16 gene Genbank Accession Number M57289 <u>TAPITDVSLGDELRLDGEEVDMTPADALDDFDLEMLGDVESPSFGMTHDPVSYGALD</u> <u>VDDFEFEQMFTDALGIDDFG</u>	63
Herpes simplex virus type 2 VP16 gene Genbank Accession Number M57289 ADALDDFDLEMADALDDFDLEMADALDDFDLEMADALDDFDLEM	64